

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/807,201

CRF Processing Date: 12/2/2001
 Edited by: [Signature]
 Verified by: [Signature]

ENTERED

1600 1642

RECEIVED
 DEC 16 2002
 STIC Staff
 P#13

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



1600

RAW SEQUENCE LISTING

DATE: 12/12/2002

PATENT APPLICATION: US/09/807,201

TIME: 20:01:02

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12122002\I807201.raw

3 <110> APPLICANT: Salceda, Susana
 4 Recipon, Herve
 5 Cafferkey, Robert
 7 <120> TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and
 Treating Prostate
 8 Cancer
 10 <130> FILE REFERENCE: DEX-0196
 12 <140> CURRENT APPLICATION NUMBER: US 09/807,201
 13 <141> CURRENT FILING DATE: 2001-04-25
 15 <150> PRIOR APPLICATION NUMBER: PCT/US99/24331
 16 <151> PRIOR FILING DATE: 1999-10-19
 18 <150> PRIOR APPLICATION NUMBER: US 60/104,737
 19 <151> PRIOR FILING DATE: 1998-10-19
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366	atttgagac	cgaagactgg	gatgcctgtc	ttgagtagac	ttggacccaa	aaaatcatct	9660
368	caccttgagc	ccacccccac	cccattgtct	aatctgtaga	agctaataaa	taatcatccc	9720

RAW SEQUENCE LISTING

DATE: 12/12/2002

PATENT APPLICATION: US/09/807,201

TIME: 20:01:02

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12122002\I807201.raw

```

370 tccttgcccta gcataacaga gaatcctttt tttaacgggtg atgcgctgta gaaatgtgac 9780
372 tagattttct cattggttct gccctcaagc actgaattc 9819
375 <210> SEQ ID NO: 3
376 <211> LENGTH: 250
377 <212> TYPE: DNA
378 <213> ORGANISM: Homo sapiens
380 <400> SEQUENCE: 3
381 cgcccctgcg ccgccgagcc agctgccaga atgccgaact ggggaggagg caagaaatgt 60
383 ggggtgtgtc agaagacggg ttactttgcc gaagagggtc agtgccaagg caacagcttc 120
385 cataaatcct gcttcctgtg catggctctg aagaagaatc tggacagtac cactgtggcc 180
387 gtgcatgggt aggagattta ctgcaagtcc tgctacggca agaagtatgg gcccaaaggc 240
389 tatggctacg 250
392 <210> SEQ ID NO: 4
393 <211> LENGTH: 1900
394 <212> TYPE: DNA
395 <213> ORGANISM: Homo sapiens
397 <220> FEATURE:
398 <221> NAME/KEY: misc_feature
399 <222> LOCATION: (16)..(16) /
400 <223> OTHER INFORMATION: n=a, c, g or t
403 <220> FEATURE:
404 <221> NAME/KEY: misc_feature
405 <222> LOCATION: (18)..(18) /
406 <223> OTHER INFORMATION: n=a, c, g or t
409 <220> FEATURE:
410 <221> NAME/KEY: misc_feature
411 <222> LOCATION: (20)..(20) /
412 <223> OTHER INFORMATION: n=a, c, g or t
415 <220> FEATURE:
416 <221> NAME/KEY: misc_feature
417 <222> LOCATION: (1887)..(1887)
418 <223> OTHER INFORMATION: n=a, c, g or t
421 <220> FEATURE:
422 <221> NAME/KEY: misc_feature
423 <222> LOCATION: (1894)..(1894)
424 <223> OTHER INFORMATION: n=a, c, g or t
427 <400> SEQUENCE: 4
W--> 428 acgccttcgg cggagnanan caaaacggcg cgcaggccgg gcgcacccag ccgccacttc 60
430 cgagagcgcc tgccgcccct ggccgcccgg agccagctgc cagaatgccg aactggggag 120
432 gaggcaagaa atgtgggggtg tgtcaagaag acggtttact ttgccgaaga ggttcagtgc 180
434 gaaggcaaca gcttcataa atcctgcttc ctgtgcatgg tctgcaagaa gaatctggac 240
436 agtaccactg tgggccgtgc atggtgagga gatttactgg caagtccttg ctacggcaag 300
438 aagtatgggc ccaaaggcta tggctacggg ccagggcgca ggcaccctca gcaactgaca 360
440 gggggagtcg ctgggtatca agcacgagga agcccctggg ccacaggccc accaccaacc 420
442 ccaatggcat ccaaatttgc ccagaagatt ggtggctccg agcgctgccc ccgatgcagc 480
444 caggcagtc atgctgcgga gaaggtgatt ggtgctggga agtcctggca taaggcctgc 540
446 ttctgatgtg ccaagtgtgg caaaggcctt gagtcaacca ccctgggcag acaaggatgg 600
448 cgagatttac tgcaaaggat gttatgctaa aaacttcggg cccaagggct ttggttttgg 660
450 gcaaggagct ggggccttgg tccactctga gtgaggccac catcaccac cacaccctgc 720

```

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 12/12/2002

PATENT APPLICATION: US/09/807,201

TIME: 20:01:03

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12122002\I807201.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 16,18,20,1887,1894

Seq#:10; N Pos. 4131,5117,5552

Seq#:13; N Pos. 4

Seq#:17; N Pos. 191

Seq#:20; N Pos. 287

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,201

DATE: 12/12/2002

TIME: 10:32:54

Input Set : A:\PTO.txt

Output Set: N:\CRF4\12122002\I807201.raw

3 <110> APPLICANT: Salceda, Susana
 4 Recipon, Herve
 5 Cafferkey, Robert
 7 <120> TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and
 Treating Prostate
 8 Cancer
 10 <130> FILE REFERENCE: DEX-0196
 12 <140> CURRENT APPLICATION NUMBER: US 09/807,201
 13 <141> CURRENT FILING DATE: 2001-04-25
 15 <150> PRIOR APPLICATION NUMBER: PCT/US99/24331
 16 <151> PRIOR FILING DATE: 1999-10-19
 18 <150> PRIOR APPLICATION NUMBER: US 60/104,737
 19 <151> PRIOR FILING DATE: 1998-10-19
 21 <160> NUMBER OF SEQ ID NOS: 36
 23 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

1595 <210> SEQ ID NO: 36
 1596 <211> LENGTH: 21
 1597 <212> TYPE: DNA
 1598 <213> ORGANISM: Artificial Sequence
 1600 <220> FEATURE:
 1601 <223> OTHER INFORMATION: Synthetic
 1603 <400> SEQUENCE: 36
 1604 cgtggagatg gctctgatgt a
 E--> 1609 (21)

**Does Not Comply
 Corrected Diskette Needed**

21

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/807,201

DATE: 12/12/2002
TIME: 10:32:56

Input Set : A:\PTO.txt
Output Set: N:\CRF4\12122002\I807201.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

VERIFICATION SUMMARY

DATE: 12/12/2002

PATENT APPLICATION: US/09/807,201

TIME: 10:32:56

Input Set : A:\PTO.txt

Output Set: N:\CRF4\12122002\I807201.raw

L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1860
L:936 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:4080
L:970 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:5100
L:984 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:5520
L:1219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:1351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:180
L:1412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:240
L:1609 M:254 E: No. of Bases conflict, this line has no nucleotides.